

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 12:43:21 ; Search time 14.7273 Seconds
(without alignments)
1085.979 Million cell updates/sec

Title: US-10-080-839-12
Perfect score: 1988
Sequence: 1 SAKGIDYDKLIVRFGSSKID.....VTDEIVKEFMTPRKLSFDFQ 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SEQ NO: 12
Summary

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	Query	Match	Length	DB	ID	
No.	Score					
1	1195.5	60.1	424	3	US-08-876-885-26	Sequence 26, Appl
2	195	9.8	338	4	US-09-328-352-4201	Sequence 4201, Ap
3	186	9.4	348	4	US-09-107-532A-5765	Sequence 5765, Ap
4	185.5	9.3	341	3	US-08-928-100-2	Sequence 2, Appli
5	185.5	9.3	341	4	US-09-492-581-2	Sequence 2, Appli
6	185.5	9.3	341	4	US-09-425-666-2	Sequence 2, Appli
7	164.5	8.3	409	2	US-08-743-130A-39	Sequence 39, Appl
8	162.5	8.2	409	2	US-08-743-130A-2	Sequence 2, Appli
9	152	7.6	344	4	US-09-198-452A-857	Sequence 857, App
10	132.5	6.7	388	2	US-08-705-868-4	Sequence 4, Appli
11	132.5	6.7	388	3	US-09-123-615-4	Sequence 4, Appli

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OM protein - protein search, using sw model

Run on: February 20, 2004, 12:46:42 ; Search time 28.9636 Seconds
(without alignments)
2732.616 Million cell updates/sec

Title: US-10-080-839-12
Perfect score: 1988
Sequence: 1 SAKGIDYDKLIVRFGSSKID.....VTDEIVKEFMTPRKLSFDFQ 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1988	100.0	392	10	US-09-813-718-16	Sequence 16, Appl
2	1988	100.0	392	12	US-10-240-532-16	Sequence 16, Appl
3	1988	100.0	415	10	US-09-813-718-14	Sequence 14, Appl
4	1988	100.0	415	12	US-10-240-532-14	Sequence 14, Appl
5	1988	100.0	437	10	US-09-813-718-12	Sequence 12, Appl
6	1988	100.0	437	12	US-10-240-532-12	Sequence 12, Appl
7	1988	100.0	471	12	US-10-295-027-1234	Sequence 1234, Ap
8	1988	100.0	471	15	US-10-1262-467B-2	Sequence 2, Appli
9	1988	100.0	484	10	US-09-813-718-10	Sequence 10, Appl
10	1988	100.0	484	12	US-10-240-532-10	Sequence 10, Appl
11	1973	99.2	471	11	US-09-919-039-163	Sequence 163, App
12	1973	99.2	471	12	US-10-247-671-166	Sequence 166, App
13	1973	99.2	475	9	US-09-925-302-558	Sequence 558, App
14	1853	93.2	475	12	US-10-205-219-65	Sequence 65, Appl
15	1177.5	59.2	424	12	US-10-032-585-7632	Sequence 7632, Ap
16	1119.5	56.3	433	15	US-10-128-714-8545	Sequence 8545, Ap
17	1099	55.3	456	12	US-10-320-797-3204	Sequence 3204, Ap
18	831	41.8	173	9	US-09-925-302-855	Sequence 855, App
19	409	20.6	179	15	US-10-128-714-3545	Sequence 3545, Ap
20	228	11.5	286	12	US-09-930-512-32	Sequence 32, Appl
21	200	10.1	85	10	US-09-813-718-45	Sequence 45, Appl
22	200	10.1	85	12	US-10-240-532-45	Sequence 45, Appl
23	191	9.6	85	10	US-09-813-718-46	Sequence 46, Appl
24	191	9.6	85	12	US-10-240-532-46	Sequence 46, Appl
25	187	9.4	85	10	US-09-813-718-48	Sequence 48, Appl
26	187	9.4	85	12	US-10-240-532-48	Sequence 48, Appl
27	185.5	9.3	341	9	US-09-815-242-13444	Sequence 13444, A
28	178	9.0	85	10	US-09-813-718-47	Sequence 47, Appl
29	178	9.0	85	12	US-10-240-532-47	Sequence 47, Appl
30	164.5	8.3	409	12	US-10-032-585-7335	Sequence 7335, Ap
31	152	7.6	344	12	US-10-289-762-857	Sequence 857, App
32	147	7.4	385	15	US-10-128-714-3379	Sequence 3379, Ap
33	146.5	7.4	391	15	US-10-128-714-8379	Sequence 8379, Ap
34	146	7.3	339	9	US-09-815-242-11422	Sequence 11422, A
35	142.5	7.2	337	15	US-10-156-761-10954	Sequence 10954, A
36	141.5	7.1	399	12	US-10-320-797-3147	Sequence 3147, Ap
37	134	6.7	372	10	US-09-813-718-8	Sequence 8, Appli
38	134	6.7	372	12	US-10-240-532-8	Sequence 8, Appli
39	132.5	6.7	372	10	US-09-813-718-4	Sequence 4, Appli
40	132.5	6.7	372	12	US-10-240-532-4	Sequence 4, Appli
41	132.5	6.7	536	10	US-09-813-718-2	Sequence 2, Appli
42	132.5	6.7	536	12	US-10-240-532-2	Sequence 2, Appli
43	128	6.4	334	9	US-09-815-242-11070	Sequence 11070, A
44	119	6.0	415	12	US-09-930-512-4	Sequence 4, Appli
45	113.5	5.7	423	9	US-09-815-242-10678	Sequence 10678, A

150000
4/27/04

627066

60/222113

ALIGNMENTS

RESULT 1
US-09-813-718-16

OM protein - protein search, using sw model

Run on: February 20, 2004, 12:42:31 ; Search time 16.2 Seconds
(without alignments)
2243.936 Million cell updates/sec

Title: US-10-080-839-12
Perfect score: 1988
Sequence: 1 SAKGIDYDKLIVRFGSSKID.....VTDEIVKEFMTPRKLSFDFQ 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
1	1973	99.2	471	1	A41706	tryptophan-tRNA li		
2	1927.5	97.0	475	1	YWBO	tryptophan-tRNA li		
3	1864	93.8	475	1	YWRBPR	tryptophan-tRNA li		
4	1853	93.2	481	2	S50053	tryptophan-tRNA li		
5	1186	59.7	395	2	S58157	hypothetical prote		
6	1138.5	57.3	432	2	S51901	tryptophan-tRNA li		
7	891.5	44.8	386	2	C90190	tryptophanyl-tRNA		
8	786.5	39.6	385	2	C75020	tryptophanyl-tRNA		
9	626.5	31.5	301	2	G71206	tryptophan-tRNA li		
10	525	26.4	380	2	G84373	tryptophanyl-tRNA		
11	406.5	20.4	370	2	F64476	tryptophan-tRNA li		
12	382.5	19.2	364	2	E69131	tryptophan-tRNA li		
13	370	18.6	134	2	T43806	tryptophan-tRNA li		

OM protein - protein search, using sw model

Run on: February 20, 2004, 12:38:51 ; Search time 9.81818 Seconds
(without alignments)
1810.528 Million cell updates/sec

Title: US-10-080-839-12
Perfect score: 1988
Sequence: 1 SAKGIDYDKLIVRFGSSKID.....VTDEIVKEFMTPRKLSFDFQ 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1973	99.2	471	1	SYW_HUMAN	P23381 homo sapien
2	1927.5	97.0	475	1	SYW_BOVIN	P17248 bos taurus
3	1879	94.5	475	1	SYW_RABIT	P23612 oryctolagus
4	1853	93.2	481	1	SYW_MOUSE	P32921 mus musculu
5	1186	59.7	395	1	SYW_SCHPO	Q09692 schizosacch
6	1138.5	57.3	432	1	SYWC_YEAST	Q12109 saccharomyc
7	895.5	45.0	381	1	SYW_SULTO	Q976m1 sulfolobus
8	891.5	44.8	380	1	SYW_SULSO	Q97zx0 sulfolobus
9	809	40.7	385	1	SYW_PYRFU	Q8u453 pyrococcus
10	786.5	39.6	385	1	SYW_PYRAB	Q9uy11 pyrococcus
11	782	39.3	386	1	SYW_PYRHO	O59584 pyrococcus
12	717.5	36.1	375	1	SYW_PYRAE	Q8ztu5 pyrobaculum
13	525	26.4	380	1	SYW_HALN1	Q9hn66 halobacteri
14	434.5	21.9	374	1	SYW_METKA	Q8tyf7 methanopyru
15	406.5	20.4	370	1	SYW_METJA	Q58810 methanococc
16	382.5	19.2	364	1	SYW_METTH	O26352 methanobact
17	370	18.6	134	1	SYW_ENCCU	O96771 encephalito

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OM protein - protein search, using sw model

Run on: February 20, 2004, 12:41:56 ; Search time 30.4364 Seconds
(without alignments)
3204.847 Million cell updates/sec

Title: US-10-080-839-12
Perfect score: 1988
Sequence: 1 SAKGIDYDKLIVRFGSSKID.....VTDEIVKEFMTPRKLSFDFQ 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1872	94.2	475	11	Q9DC65	Q9dc65	mus musculu
2	1872	94.2	481	11	Q99J58	Q99j58	mus musculu
3	1537	77.3	305	11	O70184	O70184	cavia porce
4	1324.5	66.6	420	5	Q9U4Y0	Q9u4y0	drosophila
5	1324.5	66.6	430	5	Q9U4Y1	Q9u4y1	drosophila
6	1320.5	66.4	430	5	Q9VHG2	Q9vhg2	drosophila
7	1268.5	63.8	402	10	Q9SR15	Q9sr15	arabidopsis
8	1001.5	50.4	632	5	Q8IDW3	Q8idw3	plasmodium
9	980	49.3	324	5	Q9U1R2	Q9ulr2	caenorhabdi
10	926	46.6	385	5	Q8SQY5	Q8sqy5	encephalito
11	756.5	38.1	490	5	Q9U1F5	Q9ulf5	leishmania
12	682	34.3	136	6	Q95295	Q95295	sus scrofa
13	294	14.8	157	5	Q9U533	Q9u533	trypanosoma
14	293	14.7	111	5	Q95YL8	Q95yl8	encephalito
15	286	14.4	109	4	Q9UDI5	Q9udi5	homo sapien
16	283.5	14.3	136	6	Q9TS88	Q9ts88	bos taurus
17	247.5	12.4	513	17	Q9HN83	Q9hn83	halobacteri
18	203.5	10.2	341	16	Q8E2J5	Q8e2j5	streptococc
19	203.5	10.2	341	16	Q8DWP7	Q8dwp7	streptococc
20	191	9.6	324	17	Q8TXZ2	Q8txz2	methanopyru
21	188	9.5	364	17	Q9YA64	Q9ya64	aeropyrum p
22	181.5	9.1	331	17	Q979Z1	Q979z1	thermoplasm
23	181	9.1	340	16	Q8DRR1	Q8drr1	streptococc
24	171.5	8.6	351	10	P93018	P93018	arabidopsis
25	171.5	8.6	385	10	Q8S9J2	Q8s9j2	arabidopsis
26	167	8.4	351	16	Q9RVD6	Q9rvd6	deinococcus
27	164.5	8.3	895	10	Q9SGN2	Q9sgn2	arabidopsis
28	158.5	8.0	375	17	Q9V027	Q9v027	pyrococcus
29	156	7.8	372	17	Q8ZYT7	Q8zyt7	pyrobaculum
30	153.5	7.7	317	17	Q8TSI1	Q8tsi1	methanosarc
31	152.5	7.7	682	5	Q9N9B8	Q9n9b8	leishmania
32	152	7.6	317	17	Q8PVK0	Q8pvk0	methanosarc
33	149.5	7.5	327	17	Q9HN62	Q9hn62	halobacteri
34	149.5	7.5	408	10	P93363	P93363	nicotiana t
35	148	7.4	316	17	Q8ZW77	Q8zw77	pyrobaculum
36	147	7.4	344	16	Q8KGF5	Q8kgf5	chlorobium
37	146	7.3	375	17	O58739	O58739	pyrococcus
38	145.5	7.3	528	11	Q8C183	Q8c183	mus musculu
39	145	7.3	332	17	Q9HKT3	Q9hkt3	thermoplasm
40	145	7.3	337	16	Q8Z0Y0	Q8z0y0	salmonella
41	142.5	7.2	375	17	Q8U2H3	Q8u2h3	pyrococcus
42	142.5	7.2	528	11	Q91WQ3	Q91wq3	mus musculu
43	140	7.0	337	16	Q8ZK00	Q8zk00	salmonella
44	139.5	7.0	373	5	Q8IAR7	Q8iar7	plasmodium
45	139.5	7.0	528	11	Q8BVT2	Q8bvt2	mus musculu

ALIGNMENTS

RESULT 1
Q9DC65

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OM protein - protein search, using sw model

Run on: February 20, 2004, 12:38:16 ; Search time 36.8182 Seconds
(without alignments)
1629.593 Million cell updates/sec

Title: US-10-080-839-12
Perfect score: 1988
Sequence: 1 SAKGIDYDKLIVRFGSSKID.....VTDEIVKEFMTPRKLSFDFQ 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1988	100.0	378	23	AAG79541	TrpRS T2 polypepti	
2	1988	100.0	392	22	AAB47618	Human inactive Trp	
3	1988	100.0	392	23	AAG79544	His6-tagged TrpRS	
4	1988	100.0	392	23	AAE13494	Human inactive try	
5	1988	100.0	401	23	AAG79549	TrpRS T1 polypepti	
6	1988	100.0	415	22	AAB47617	Human supermini Tr	
7	1988	100.0	415	23	AAG79548	His6-tagged TrpRS	
8	1988	100.0	415	23	AAE13493	Human supermini tr	
9	1988	100.0	437	22	AAB47616	Human mini TrpRS.	
10	1988	100.0	437	23	AAG79547	His6-tagged mini-T	
11	1988	100.0	437	23	AAE13492	Human mini tryptop	
12	1988	100.0	484	22	AAB47615	Human full-length	
13	1988	100.0	484	23	AAG79546	Full length human	
14	1988	100.0	484	23	AAE13491	Human tryptophanyl	
15	1973	99.2	378	24	AAG79953	T2-TrpRS. Homo sa	
16	1973	99.2	475	21	AAB58220	Lung cancer associ	
17	1968	99.0	471	20	AAV05372	Human HCMV inducib	
18	1320.5	66.4	430	22	ABB64621	Drosophila melanog	
19	1320.5	66.4	430	22	ABB67203	Drosophila melanog	
20	1271.5	64.0	402	21	AAG23698	Arabidopsis thalia	
21	1271.5	64.0	426	21	AAG23697	Arabidopsis thalia	
22	1195.5	60.1	424	22	AAB66931	Tryptophanyl-tRNA	
23	1177.5	59.2	424	23	ABP73795	Candida albicans e	
24	1119.5	56.3	433	24	ABJ26487	Aspergillus fumiga	
25	968	48.7	292	21	AAG23699	Arabidopsis thalia	
26	831	41.8	173	21	AAB58517	Lung cancer associ	
27	786.5	39.6	385	22	AAB96409	Putative P. abyssi	
28	409	20.6	179	24	ABJ25887	Aspergillus fumiga	
29	203.5	10.2	341	23	ABP26964	Streptococcus poly	
30	200	10.1	85	23	AAE13515	Human tryptophanyl	
31	191	9.6	39	24	AAG79951	T2-TrpRS partial s	
32	185.5	9.3	341	19	AAW56423	Tryptophanyl tRNA	
33	185.5	9.3	341	22	AAU37851	Streptococcus pneu	
34	185.5	9.3	341	24	ABU02760	S. pneumoniae type	
35	182.5	9.2	341	23	ABP26965	Streptococcus poly	
36	174.5	8.8	341	23	ABB53366	Lactococcus lactis	
37	164.5	8.3	409	20	AAW94248	C. albicans tyrosy	
38	164.5	8.3	409	23	ABP73498	Candida albicans e	
39	162.5	8.2	409	20	AAW94247	C. albicans tyrosy	
40	159.5	8.0	379	20	AAV37623	Protein involved i	
41	158.5	8.0	378	22	AAB96600	Putative P. abyssi	
42	152	7.6	344	20	AAV35439	Chlamydia pneumoni	
43	147	7.4	385	24	ABJ25721	Aspergillus fumiga	
44	146.5	7.4	391	24	ABJ26321	Aspergillus fumiga	
45	146	7.3	339	22	AAU35829	Helicobacter pylor	

ALIGNMENTS